

ABSTRACT

The invention provides several methods for reducing the complexity of a population of nucleic acids prior to performing an analysis of the nucleic acids on a nucleic acid probe array. The methods result in a subset of the initial population enriched for a desired property, or lacking nucleic acids having an undesired property. The resulting nucleic acids in the subset are then applied to the array for various types of analysis. The methods are particularly useful for analyzing populations having a high degree of complexity, for example, chromosomal-derived DNA, or whole genomic DNA, or mRNA population. In addition, such methods allow for analysis of pooled samples.